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RAW SEQUENCE LISTING

DATE: 11/28/2001

PATENT APPLICATION: US/09/921,650B

TIME: 18:10:13

Input Set : A:\09921650A.raw.txt

Output Set: N:\CRF3\11212001\I921650B.raw

SEQUENCE LISTING

ENTERED

1 (1) GENERAL INFORMATION:
2 (i) APPLICANT: Bujard, Hermann
3 Gossen, Manfred
4 (ii) TITLE OF INVENTION: Tetracycline-Inducible Transcriptional
5 Inhibitor Fusion Proteins
6 (iii) NUMBER OF SEQUENCES: 37
7 (iv) CORRESPONDENCE ADDRESS:
8 (A) ADDRESSEE: LAHIVE & COCKFIELD
9 (B) STREET: 28 State Street
10 (C) CITY: Boston
11 (D) STATE: Massachusetts
12 (E) COUNTRY: USA
13 (F) ZIP: 02109-1875
14 (v) COMPUTER READABLE FORM:
15 (A) MEDIUM TYPE: Floppy disk
16 (B) COMPUTER: IBM PC compatible
17 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
18 (D) SOFTWARE: ASCII Text
19 (vi) CURRENT APPLICATION DATA:
C--> 20 (A) APPLICATION NUMBER: US/09/921,650B
C--> 21 (B) FILING DATE: 03-Aug-2001
22 (C) CLASSIFICATION:
23 (vii) PRIOR APPLICATION DATA:
24 (A) APPLICATION NUMBER: US/09/489,777
25 (B) FILING DATE: 24-Jan-2000
26 (A) APPLICATION NUMBER: US 09/162,184
27 (B) FILING DATE: 28-SEP-1998
28 (A) APPLICATION NUMBER: US 08/485,978
29 (B) FILING DATE: 07-JUN-1995
30 (A) APPLICATION NUMBER: US 08/383,754
31 (B) FILING DATE: 03-FEB-1995
32 (A) APPLICATION NUMBER: US 08/275,876
33 (B) FILING DATE: 15-JULY-1994
34 (A) APPLICATION NUMBER: US 08/270,637
35 (B) FILING DATE: 01-JULY-1994
36 (A) APPLICATION NUMBER: US 08/260,452
37 (B) FILING DATE: 14-JUNE-1994
38 (A) APPLICATION NUMBER: US 08/076,327
39 (B) FILING DATE: 14-JUNE-1993
40 (A) APPLICATION NUMBER: US 08/076,726
41 (B) FILING DATE: 14-JUNE-1993
42 (viii) ATTORNEY/AGENT INFORMATION:
43 (A) NAME: DeConti, Giulio A. Jr.
44 (B) REGISTRATION NUMBER: 31,503
45 (C) REFERENCE/DOCKET NUMBER: BBI-009C6CNDV
46 (ix) TELECOMMUNICATION INFORMATION:

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```

47      (A) TELEPHONE: (617)227-7400
48      (B) TELEFAX: (617)742-4214
49 (2) INFORMATION FOR SEQ ID NO: 1:
50      (i) SEQUENCE CHARACTERISTICS:
51          (A) LENGTH: 1008 base pairs
52          (B) TYPE: nucleic acid
53          (C) STRANDEDNESS: double
54          (D) TOPOLOGY: linear
W--> 55      (ii) MOLECULE TYPE: DNA
56      (ix) FEATURE:
57          (A) NAME/KEY: exon
58          (B) LOCATION: 1..1008
59      (ix) FEATURE:
60          (A) NAME/KEY: mRNA
61          (B) LOCATION: 1..1008
62      (ix) FEATURE:
63          (A) NAME/KEY: misc. binding
64          (B) LOCATION: 1..207
65      (ix) FEATURE:
66          (A) NAME/KEY: misc. binding
67          (B) LOCATION: 208..335
68      (ix) FEATURE:
69          (A) NAME/KEY: CDS
70          (B) LOCATION: 1..1005
71      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72      ATG TCT AGA TTA GAT AAA AGT AAA GTG ATT AAC AGC GCA TTA GAG CTG      48
73      Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
74      1          5          10          15
75      CTT AAT GAG GTC GGA ATC GAA GGT TTA ACA ACC CGT AAA CTC GCC CAG      96
76      Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln
77      20          25          30
78      AAG CTA GGT GTA GAG CAG CCT ACA CTG TAT TGG CAT GTA AAA AAT AAG      144
79      Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
80      35          40          45
81      CGG GCT TTG CTC GAC GCC TTA GCC ATT GAG ATG TTA GAT AGG CAC CAT      192
82      Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
83      50          55          60
84      ACT CAC TTT TGC CCT TTA AAA GGG GAA AGC TGG CAA GAT TTT TTA CGC      240
85      Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
86      65          70          75          80
87      AAT AAG GCT AAA AGT TTT AGA TGT GCT TTA CTA AGT CAT CGC AAT GGA      288
88      Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
89      85          90          95
90      GCA AAA GTA CAT TCA GAT ACA CGG CCT ACA GAA AAA CAG TAT GAA ACT      336
91      Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
92      100          105          110
93      CTC GAA AAT CAA TTA GCC TTT TTA TGC CAA CAA GGT TTT TCA CTA GAG      384
94      Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
95      115          120          125

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96  AAT GCA TTA TAT GCA CTC AGC GCT GTG GGG CAT TTT ACT TTA GGT TGC      432
97  Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
98      130                      135                      140
99  GTA TTG GAA GAT CAA GAG CAT CAA GTC GCT AAA GAA GAA AGG GAA ACA      480
100  Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
101      145                      150                      155                      160
102  CCT ACT ACT GAT AGT ATG CCG CCA TTA TTA CGA CAA GCT ATC GAA TTA      528
103  Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
104                      165                      170                      175
105  TTT GAT CAC CAA GGT GCA GAG CCA GCC TTC TTA TTC GGC CTT GAA TTG      576
106  Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
107                      180                      185                      190
108  ATC ATA TGC GGA TTA GAA AAA CAA CTT AAA TGT GAA AGT GGG TCC GCG      624
109  Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
110                      195                      200                      205
111  TAC AGC CGC GCG CGT ACG AAA AAC AAT TAC GGG TCT ACC ATC GAG GGC      672
112  Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
113      210                      215                      220
114  CTG CTC GAT CTC CCG GAC GAC GAC GCC CCC GAA GAG GCG GGG CTG GCG      720
115  Leu Leu Asp Leu Pro Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
116      225                      230                      235                      240
117  GCT CCG CGC CTG TCC TTT CTC CCC GCG GGA CAC ACG CGC AGA CTG TCG      768
118  Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
119                      245                      250                      255
120  ACG GCC CCC CCG ACC GAT GTC AGC CTG GGG GAC GAG CTC CAC TTA GAC      816
121  Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
122                      260                      265                      270
123  GGC GAG GAC GTG GCG ATG GCG CAT GCC GAC GCG CTA GAC GAT TTC GAT      864
124  Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
125                      275                      280                      285
126  CTG GAC ATG TTG GGG GAC GGG GAT TCC CCG GGT CCG GGA TTT ACC CCC      912
127  Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
128      290                      295                      300
129  CAC GAC TCC GCC CCC TAC GGC GCT CTG GAT ATG GCC GAC TTC GAG TTT      960
130  His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
131      305                      310                      315                      320
132  GAG CAG ATG TTT ACC GAT CCC CTT GGA ATT GAC GAG TAC GGT GGG TAG      1008
133  Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
134                      325                      330                      335

136 (2) INFORMATION FOR SEQ ID NO: 2:
137     (i) SEQUENCE CHARACTERISTICS:
138         (A) LENGTH: 335 amino acids
139         (B) TYPE: amino acid
140         (D) TOPOLOGY: linear
141     (ii) MOLECULE TYPE: protein
142     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
143     Met Ser Arg Leu Asp Lys Ser Lys Val Ile Asn Ser Ala Leu Glu Leu
144         1             5             10             15
145     Leu Asn Glu Val Gly Ile Glu Gly Leu Thr Thr Arg Lys Leu Ala Gln

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146          20          25          30
147 Lys Leu Gly Val Glu Gln Pro Thr Leu Tyr Trp His Val Lys Asn Lys
148          35          40          45
149 Arg Ala Leu Leu Asp Ala Leu Ala Ile Glu Met Leu Asp Arg His His
150          50          55          60
151 Thr His Phe Cys Pro Leu Lys Gly Glu Ser Trp Gln Asp Phe Leu Arg
152          65          70          75          80
153 Asn Lys Ala Lys Ser Phe Arg Cys Ala Leu Leu Ser His Arg Asn Gly
154          85          90          95
155 Ala Lys Val His Ser Asp Thr Arg Pro Thr Glu Lys Gln Tyr Glu Thr
156          100          105          110
157 Leu Glu Asn Gln Leu Ala Phe Leu Cys Gln Gln Gly Phe Ser Leu Glu
158          115          120          125
159 Asn Ala Leu Tyr Ala Leu Ser Ala Val Gly His Phe Thr Leu Gly Cys
160          130          135          140
161 Val Leu Glu Asp Gln Glu His Gln Val Ala Lys Glu Glu Arg Glu Thr
162          145          150          155          160
163 Pro Thr Thr Asp Ser Met Pro Pro Leu Leu Arg Gln Ala Ile Glu Leu
164          165          170          175
165 Phe Asp His Gln Gly Ala Glu Pro Ala Phe Leu Phe Gly Leu Glu Leu
166          180          185          190
167 Ile Ile Cys Gly Leu Glu Lys Gln Leu Lys Cys Glu Ser Gly Ser Ala
168          195          200          205
169 Tyr Ser Arg Ala Arg Thr Lys Asn Asn Tyr Gly Ser Thr Ile Glu Gly
170          210          215          220
171 Leu Leu Asp Leu Pro Asp Asp Asp Ala Pro Glu Glu Ala Gly Leu Ala
172          225          230          235          240
173 Ala Pro Arg Leu Ser Phe Leu Pro Ala Gly His Thr Arg Arg Leu Ser
174          245          250          255
175 Thr Ala Pro Pro Thr Asp Val Ser Leu Gly Asp Glu Leu His Leu Asp
176          260          265          270
177 Gly Glu Asp Val Ala Met Ala His Ala Asp Ala Leu Asp Asp Phe Asp
178          275          280          285
179 Leu Asp Met Leu Gly Asp Gly Asp Ser Pro Gly Pro Gly Phe Thr Pro
180          290          295          300
181 His Asp Ser Ala Pro Tyr Gly Ala Leu Asp Met Ala Asp Phe Glu Phe
182          305          310          315          320
183 Glu Gln Met Phe Thr Asp Pro Leu Gly Ile Asp Glu Tyr Gly Gly
184          325          330          335

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186 (2) INFORMATION FOR SEQ ID NO: 3:

187 (i) SEQUENCE CHARACTERISTICS:

188 (A) LENGTH: 33 base pairs

189 (B) TYPE: nucleic acid

190 (C) STRANDEDNESS: double

191 (D) TOPOLOGY: linear

W--> 192 (ii) MOLECULE TYPE: DNA

193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

194 GAC GCG CTA GAC GAT TTC GAT CTG GAC ATG TTG 33

195 Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu

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196          1          5          10
198 (2) INFORMATION FOR SEQ ID NO: 4:
199     (i) SEQUENCE CHARACTERISTICS:
200         (A) LENGTH: 11 amino acids
201         (B) TYPE: amino acid
202         (D) TOPOLOGY: linear
203     (ii) MOLECULE TYPE: peptide
204     (v) FRAGMENT TYPE: internal
205     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
206         Asp Ala Leu Asp Asp Phe Asp Leu Asp Met Leu
207         1          5          10
209 (2) INFORMATION FOR SEQ ID NO: 5:
210     (i) SEQUENCE CHARACTERISTICS:
211         (A) LENGTH: 7 amino acids
212         (B) TYPE: amino acid
213         (D) TOPOLOGY: linear
214     (ii) MOLECULE TYPE: peptide
215     (v) FRAGMENT TYPE: internal
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
217         Met Pro Lys Arg Pro Arg Pro
218         1          5
220 (2) INFORMATION FOR SEQ ID NO: 6:
221     (i) SEQUENCE CHARACTERISTICS:
222         (A) LENGTH: 569 base pairs
223         (B) TYPE: nucleic acid
224         (C) STRANDEDNESS: double
225         (D) TOPOLOGY: linear
W--> 226     (ii) MOLECULE TYPE: DNA
227     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
228         GAATTCGGGG CCGCGGAGGC TGGATCGGTC CCGGTGTCTT CTATGGAGGT CAAAACAGCG      60
229         TGGATGGCGT CTCCAGGCGA TCTGACGGTT CACTAAACGA GCTCTGCTTA TATAGGTCGA      120
230         GTTTACCACT CCCTATCAGT GATAGAGAAA AGTGAAAGTC GAGTTTACCA CTCCCTATCA      180
231         GTGATAGAGA AAAGTGAAAG TCGAGTTTAC CACTCCCTAT CAGTGATAGA GAAAAGTGAA      240
232         AGTCGAGTTT ACCACTCCCT ACCAGTGATA GAGAAAAGTG AAAGTCGAGT TTACCACTCC      300
233         CTATCAGTGA TAGAGAAAAG TGAAAGTCGA GTTTACCACT CCCTATCAGT GATAGAGAAA      360
234         AGTGAAAGTC GAGTTTACCA CTCCCTATCA GTGATAGAGA AAAGTGAAAG TCGAGCTCGG      420
235         TACCCGGGTC GAGTAGGCGT GTACGGTGGG AGGCCTATAT AAGCAGAGCT CGTTTAGTGA      480
236         ACCGTCAGAT CGCCTGGAGA CGCCATCCAC GCTGTTTGA CCTCCATAGA AGACACCGGG      540
237         ACCGATCCAG CCTCCGCGGC CCCGAATTC      569
239 (2) INFORMATION FOR SEQ ID NO: 7:
240     (i) SEQUENCE CHARACTERISTICS:
241         (A) LENGTH: 520 base pairs
242         (B) TYPE: nucleic acid
243         (C) STRANDEDNESS: double
244         (D) TOPOLOGY: linear
W--> 245     (ii) MOLECULE TYPE: DNA
246     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
247         AGATCTGCAG GGTGCTCGG TGTCGAGGC CACACGCGTC ACCTTAATAT GCGAAGTGGA      60
248         CCGGATCTCG AGTTTACCAC TCCCTATCAG TGATAGAGAA AAGTGAAAGT CGAGTTTACC      120

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VERIFICATION SUMMARY

DATE: 11/28/2001

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TIME: 18:10:14

Input Set : A:\09921650A.raw.txt

Output Set: N:\CRF3\11212001\I921650B.raw

L:20 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:21 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:55 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1
L:192 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=3
L:226 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6
L:245 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:328 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=11
L:338 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=12
L:348 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=13
L:358 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=14
L:368 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=15
L:681 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=24
L:691 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=25
L:712 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=27